



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/619,047 B

Source: 1652

Date Processed by STIC: 5-3-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY =

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Sequence Listing Error Summary

#11

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/619,047B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☒ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☐ Use of <220>Feature (NEW RULES)      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

## RAW SEQUENCE LISTING

DATE: 05/03/2001

PATENT APPLICATION: US/09/619,047B

TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt

Output Set: N:\CRF3\05032001\I619047B.raw

Does Not Comply  
Corrected Diskette Needed  
See p. 5

3 <110> APPLICANT: Chemicon International, Inc.  
4 LENG, Jay  
6 <120> TITLE OF INVENTION: PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF USE THEREOF  
8 <130> FILE REFERENCE: CHEM1110  
10 <140> CURRENT APPLICATION NUMBER: US 09/619,047B  
11 <141> CURRENT FILING DATE: 2000-07-18  
13 <160> NUMBER OF SEQ ID NOS: 29  
15 <170> SOFTWARE: PatentIn version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 936  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Renilla reniformis  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (1)..(936)  
26 <400> SEQUENCE: 1

27	atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act	48
28	Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr	
29	1 5 10 15	
31	ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca	96
32	Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser	
33	20 25 30	
35	ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att	144
36	Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile	
37	35 40 45	
39	ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg	192
40	Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val	
41	50 55 60	
43	cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt	240
44	Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly	
45	65 70 75 80	
47	atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat	288
48	Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp	
49	85 90 95	
51	cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag	336
52	His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys	
53	100 105 110	
55	aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat	384
56	Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His	
57	115 120 125	
59	tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa	432
60	Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu	
61	130 135 140	
63	agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa	480
64	Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
65	145 150 155 160	
67	gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg	528

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001

TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt

Output Set: N:\CRF3\05032001\I619047B.raw

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68 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
69          165          170          175
71 gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga      576
72 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
73          180          185          190
75 aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag      624
76 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
77          195          200          205
79 aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg      672
80 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
81          210          215          220
83 tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat      720
84 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
85 225          230          235          240
87 aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa      768
88 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
89          245          250          255
91 tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag      816
92 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
93          260          265          270
95 ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa      864
96 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
97          275          280          285
99 gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag      912
100 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
101          290          295          300
103 cga gtt ctc aaa aat gaa caa taa      936
104 Arg Val Leu Lys Asn Glu Gln
105 305          310
108 <210> SEQ ID NO: 2
109 <211> LENGTH: 311
110 <212> TYPE: PRT
111 <213> ORGANISM: Renilla reniformis
113 <400> SEQUENCE: 2
115 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
116 1          5          10          15
119 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
120          20          25          30
123 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
124          35          40          45
127 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
128          50          55          60
131 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
132 65          70          75          80
135 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
136          85          90          95
139 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
140          100          105          110
143 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His

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## RAW SEQUENCE LISTING

DATE: 05/03/2001

PATENT APPLICATION: US/09/619,047B

TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt

Output Set: N:\CRF3\05032001\I619047B.raw

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144      115      120      125
147 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
148      130      135      140
151 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
152 145      150      155      160
155 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
156      165      170      175
159 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
160      180      185      190
163 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
164      195      200      205
167 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
168      210      215      220
171 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
172 225      230      235      240
175 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
176      245      250      255
179 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
180      260      265      270
183 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
184      275      280      285
187 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
188      290      295      300
191 Arg Val Leu Lys Asn Glu Gln
192 305      310
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 936
197 <212> TYPE: DNA
198 <213> ORGANISM: Renilla reniformis (mutated sequence)
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(936)
204 <400> SEQUENCE: 3
205 atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act      48
206 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
207 1      5      10      15
209 ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca      96
210 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
211      20      25      30
213 ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att      144
214 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
215      35      40      45
217 ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg      192
218 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
219      50      55      60
221 cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt      240
222 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
223 65      70      75      80
225 atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat      288

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## RAW SEQUENCE LISTING

DATE: 05/03/2001

PATENT APPLICATION: US/09/619,047B

TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt

Output Set: N:\CRF3\05032001\I619047B.raw

```

226 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
227      85      90      95
229 cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag      336
230 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
231      100      105      110
233 aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat      384
234 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
235      115      120      125
237 tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa      432
238 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
239      130      135      140
241 agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa      480
242 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
243 145      150      155      160
245 gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg      528
246 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
247      165      170      175
249 gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga      576
250 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
251      180      185      190
253 aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag      624
254 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
255      195      200      205
257 aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg      672
258 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
259      210      215      220
261 tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat      720
262 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
263 225      230      235      240
265 aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa      768
266 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
267      245      250      255
269 tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag      816
270 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
271      260      265      270
273 ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa      864
274 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
275      275      280      285
277 gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag      912
278 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
279      290      295      300
281 cga gtt ctc aaa aat gaa caa taa      936
282 Arg Val Leu Lys Asn Glu Gln
283 305      310
286 <210> SEQ ID NO: 4
287 <211> LENGTH: 311
288 <212> TYPE: PRT
289 <213> ORGANISM: Renilla reniformis (mutated sequence)
291 <400> SEQUENCE: 4

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001  
TIME: 12:57:17

Input Set : A:\CHEM1110.ST25.txt  
Output Set: N:\CRF3\05032001\I619047B.raw

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293 Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
294 1 5 10 15
297 Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
298 20 25 30
301 Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
302 35 40 45
305 Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
306 50 55 60
309 Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
310 65 70 75 80
313 Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
314 85 90 95
317 His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
318 100 105 110
321 Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
322 115 120 125
325 Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
326 130 135 140
329 Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
330 145 150 155 160
333 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
334 165 170 175
337 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
338 180 185 190
341 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu
342 195 200 205
345 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
346 210 215 220
349 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
350 225 230 235 240
353 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
354 245 250 255
357 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
358 260 265 270
361 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
362 275 280 285
365 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
366 290 295 300
369 Arg Val Leu Lys Asn Glu Gln
370 305 310

```

373 <210> SEQ ID NO: 5  
 374 <211> LENGTH: 8  
 375 <212> TYPE: PRT  
 C--> 376 <213> ORGANISM: Artificial  
 378 <220> FEATURE:  
 379 <223> OTHER INFORMATION: Description of Artificial Sequence: Protease recognition sequence  
 381 <400> SEQUENCE: 5  
 383 Ser Gln Asn Tyr Pro Ile Val Gln  
 384 1 5

*Incomplete response as per section 1.8236 of new sequence rules. See # 11 on the Error Summary Sheet.*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. Sequences 5-29.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/619,047B

DATE: 05/03/2001

TIME: 12:57:18

Input Set : A:\CHEM1110.ST25.txt

Output Set: N:\CRF3\05032001\I619047B.raw

L:376 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:389 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6  
L:402 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7  
L:415 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:428 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:441 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:467 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:480 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:496 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:509 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:522 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:535 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:548 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:561 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19  
L:574 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20  
L:587 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21  
L:600 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22  
L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:619 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:638 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24  
L:651 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25  
L:664 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26  
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27  
L:696 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28  
L:709 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29





RECEIVED

MAY 07 2001

## SEQUENCE LISTING

TECH CENTER 1600/2900

<110> Chemicon International, Inc.  
LENG, Jay

<120> PROTEASE SPECIFIC CLEAVABLE LUCIFERASES AND METHODS OF USE THEREOF

<130> CHEM1110

<140> US 09/619,047

<141> 2000-07-18

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 936

<212> DNA

<213> Renilla reniformis

<220>

<221> CDS

<222> (1)..(936)

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1 5 10 15

ggc ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca 96  
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser  
20 25 30

ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att 144  
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
35 40 45

ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg 192  
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
50 55 60

cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt 240  
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
65 70 75 80

atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat 288  
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
85 90 95

cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag 336  
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
100 105 110

aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat 384  
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
115 120 125

tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa 432  
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
130 135 140

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agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa      480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145                      150                      155                      160

gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg      528
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
                      165                      170                      175

gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga      576
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
                      180                      185                      190

aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca ttc aaa gag      624
Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
                      195                      200                      205

aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg      672
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
                      210                      215                      220

tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat      720
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
225                      230                      235                      240

aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa      768
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
                      245                      250                      255

tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag      816
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
                      260                      265                      270

ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa      864
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
                      275                      280                      285

gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag      912
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
                      290                      295                      300

cga gtt ctc aaa aat gaa caa taa      936
Arg Val Leu Lys Asn Glu Gln
305                      310

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<210> 2
<211> 311
<212> PRT
<213> Renilla reniformis

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<400> 2

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Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
1                      5                      10                      15

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Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
20                      25                      30

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Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
 35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val  
 50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly  
 65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp  
 85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys  
 100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His  
 115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu  
 130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu  
 145 150 155 160

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu  
 165 170 175

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg  
 180 185 190

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu  
 195 200 205

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro  
 210 215 220

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr  
 225 230 235 240

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu  
 245 250 255

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys  
 260 265 270

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln

275	280	285	
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu			
290	295	300	
Arg Val Leu Lys Asn Glu Gln			
305	310		
<210>	3		
<211>	936		
<212>	DNA		
<213>	Renilla reniformis (mutated sequence)		
<220>			
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<222>	(1)..(936)		
<400>	3		
atg act tcg aaa gtt tat gat cca gaa caa agg aaa cgg atg ata act			48
Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr			
1	5	10	15
ggg ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt ctt gat tca			96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser			
	20	25	30
ttt att aat tat tat gat tca gaa aaa cat gca gaa aat gct gtt att			144
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile			
	35	40	45
ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga cat gtt gtg			192
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val			
	50	55	60
cca cat att gag cca gta gcg cgg tgt att ata cca gat ctt att ggt			240
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly			
65	70	75	80
atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg tta ctt gat			288
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp			
	85	90	95
cat tac aaa tat ctt act gca tgg ttt gaa ctt ctt aat tta cca aag			336
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys			
	100	105	110
aag atc att ttt gtc ggc cat gat tgg ggt gct tgt ttg gca ttt cat			384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His			
	115	120	125
tat agc tat gag cat caa gat aag atc aaa gca ata gtt cac gct gaa			432
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu			
	130	135	140
agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct gat att gaa			480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu			
145	150	155	160

gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa atg gtt ttg 528  
 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu  
                             165                            170                            175

gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa atc atg aga 576  
 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg  
                             180                            185                            190

aag tta gaa cca gac gaa gtt gac gca tat ctt gaa cca ttc aaa gag 624  
 Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu  
                             195                            200                            205

aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt gaa atc ccg 672  
 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro  
                             210                            215                            220

tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt agg aat tat 720  
 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr  
                             225                            230                            235                            240

aat gct tat cta cgt gca agt gat gat tta cca aaa atg ttt att gaa 768  
 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu  
                             245                            250                            255

tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc gcc aag aag 816  
 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys  
                             260                            265                            270

ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat ttt tcg caa 864  
 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln  
                             275                            280                            285

gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg ttc gtt gag 912  
 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu  
                             290                            295                            300

cga gtt ctc aaa aat gaa caa taa 936  
 Arg Val Leu Lys Asn Glu Gln  
                             305                            310

<210> 4  
 <211> 311  
 <212> PRT  
 <213> Renilla reniformis (mutated sequence)

<400> 4

Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr  
 1                            5                            10                            15

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser  
                             20                            25                            30

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile  
                             35                            40                            45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val

50		55		60
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly				
65		70		75 80
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp				
	85		90	95
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys				
	100		105	110
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His				
	115		120	125
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu				
	130		135	140
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu				
145		150	155	160
Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu				
	165		170	175
Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg				
	180		185	190
Lys Leu Glu Pro Asp Glu Val Asp Ala Tyr Leu Glu Pro Phe Lys Glu				
	195		200	205
Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro				
	210		215	220
Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr				
225		230	235	240
Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu				
	245		250	255
Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys				
	260		265	270
Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln				
	275		280	285
Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu				
	290		295	300

Arg Val Leu Lys Asn Glu Gln  
305 310

<210> 5  
<211> 8  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial sequence: Protease recognition sequence

<400> 5

Ser Gln Asn Tyr Pro Ile Val Gln  
1 5

<210> 6  
<211> 10  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial sequence: Protease recognition sequence

<400> 6

Lys Ala Arg Val Leu Ala Glu Ala Met Ser  
1 5 10

<210> 7  
<211> 10  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial sequence: Protease recognition sequence

<400> 7

Pro Ser Pro Arg Glu Gly Lys Arg Ser Tyr  
1 5 10

<210> 8  
<211> 5  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial sequence: Protease recognition sequence

<400> 8

Tyr Val Ala Asp Gly  
1 5

<210> 9  
<211> 8  
<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 9

Met Phe Gly Gly Ala Lys Lys Arg  
1 5

<210> 10

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 10

Gly Val Val Asn Ala Ser Ser Arg Leu Ala  
1 5 10

<210> 11

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 11

Leu Ile Ala Tyr Leu Lys Lys Ala Thr  
1 5

<210> 12

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 12

Val Lys Met Asp Ala Glu Phe  
1 5

<210> 13

<211> 17

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 13

Phe Leu Ala Glu Gly Gly Gly Val Arg Gly Pro Arg Val Val Glu Arg  
1 5 10 15



His

<210> 14  
 <211> 13  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence  
 <400> 14

Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His  
 1 5 10

<210> 15  
 <211> 8  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence  
 <400> 15

Lys Pro Ala Leu Phe Phe Arg Leu  
 1 5

<210> 16  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence  
 <400> 16

Ile Glu Pro Asp  
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<210> 17  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence  
 <400> 17

Asp Glu Thr Asp  
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<210> 18  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence

<400> 18

Trp Glu His Asp  
 1

<210> 19  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence

<400> 19

Tyr Val Ala Asp  
 1

<210> 20  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence

<400> 20

Asp Glu His Asp  
 1

<210> 21  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence

<400> 21

Asp Glu Val Asp  
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<210> 22  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Description of Artificial sequence: Protease recognition sequence

<220>  
 <221> VARIANT  
 <222> (1)..(1)  
 <223> Xaa is Trp or Ley

<400> 22

Xaa Glu His Asp

1

<210> 23

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<220>

<221> VARIANT

<222> (3)..(3)

<223> Xaa is Ile or His

<400> 23

Val Glu Xaa Asp

1

<210> 24

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 24

Leu Glu Thr Asp

1

<210> 25

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 25

Leu Glu His Asp

1

<210> 26

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<220>

<221> VARIANT

<222> (1)..(3)

<223> Xaa is any amino acid

<400> 26

Xaa Xaa Xaa Asp

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<210> 27

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 27

Arg Pro Leu Gly Ile Ile Gly Gly

1

5

<210> 28

<211> 3

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 28

Glu Gly Arg

1

<210> 29

<211> 3

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial sequence: Protease recognition sequence

<400> 29

Val Leu Lys

1